

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/808,052A
Source: 1fw0
Date Processed by STIC: 1/5/05

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RAW SEQUENCE LISTING

DATE: 01/05/2005

PATENT APPLICATION: US/10/808,052A

TIME: 17:00:27

Input Set : A:\18989-033.txt

Output Set: N:\CRF4\01052005\J808052A.raw

3 <110> APPLICANT: Blumberg
 5 <120> TITLE OF INVENTION: Methods of Inhibiting Inflammation
 7 <130> FILE REFERENCE: 18989-033
 9 <140> CURRENT APPLICATION NUMBER: 10/808,052A
 10 <141> CURRENT FILING DATE: 2004-03-24
 12 <150> PRIOR APPLICATION NUMBER: 60/457,048
 13 <151> PRIOR FILING DATE: 2003-03-24
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 21
 21 <212> TYPE: RNA
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically
 26 synthesized siRNA
 28 <400> SEQUENCE: 1
 29 aagcucugga acuaccaacg a 21
 32 <210> SEQ ID NO: 2
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 34 <212> TYPE: RNA
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 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Description of Artificial Sequence:chemically
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 45 <210> SEQ ID NO: 3
 46 <211> LENGTH: 3392
 47 <212> TYPE: DNA
 48 <213> ORGANISM: Homo sapiens
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 53 tttcctcata ttcagcttct gttaaaggct acacaactgg tctctcatta aataatgacc 180
 54 ggctgtacaa gctcacgtac tccactgaag ttcttcttga tcggggcaaa ggaaaactgc 240
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64 ctgaagaaac acacaatttt ggactgaatt tcctacaaac cattaagggg aaaatagtat 840
65 cgaagcagaa attagagctg aagacaaccg aagcaggccc aagattgatg tctggaaagc 900
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103 tcaacaattt ttgatcaatg tatatgaagc tcttgatagg acttccttaa gcatgacggg 3180
104 aaaaccaaac acgttcccta atcaggaaaa aaaaaaaaaa aaaaaagtaa gacacaaaca 3240
105 aaccattttt ttctcttttt ttggagttgg gggcccaggg agaagggaca aggcctttta 3300
106 aagacttggt agccaacttc aagaattaat atttatgtct ctgttattgt tagttttaag 3360
107 ccttaaggta gaaggcat agaaataaca tc 3392
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 894
112 <212> TYPE: PRT

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Input Set : A:\18989-033.txt

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115 <400> SEQUENCE: 4
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120           20           25           30
122 Leu Tyr Lys Leu Thr Tyr Ser Thr Glu Val Leu Leu Asp Arg Gly Lys
123           35           40           45
125 Gly Lys Leu Gln Asp Ser Val Gly Tyr Arg Ile Ser Ser Asn Val Asp
126           50           55           60
128 Val Ala Leu Leu Trp Arg Asn Pro Asp Gly Asp Asp Gln Leu Ile
129   65           70           75           80
131 Gln Ile Thr Met Lys Asp Val Asn Val Glu Asn Val Asn Gln Gln Arg
132           85           90           95
134 Gly Glu Lys Ser Ile Phe Lys Gly Lys Ser Pro Ser Lys Ile Met Gly
135           100          105          110
137 Lys Glu Asn Leu Glu Ala Leu Gln Arg Pro Thr Leu Leu His Leu Ile
138           115          120          125
140 His Gly Lys Val Lys Glu Phe Tyr Ser Tyr Gln Asn Glu Ala Val Ala
141           130          135          140
143 Ile Glu Asn Ile Lys Arg Gly Leu Ala Ser Leu Phe Gln Thr Gln Leu
144 145           150          155          160
146 Ser Ser Gly Thr Thr Asn Glu Val Asp Ile Ser Gly Asn Cys Lys Val
147           165          170          175
149 Thr Tyr Gln Ala His Gln Asp Lys Val Ile Lys Ile Lys Ala Leu Asp
150           180          185          190
152 Ser Cys Lys Ile Ala Arg Ser Gly Phe Thr Thr Pro Asn Gln Val Leu
153           195          200          205
155 Gly Val Ser Ser Lys Ala Thr Ser Val Thr Thr Tyr Lys Ile Glu Asp
156           210          215          220
158 Ser Phe Val Ile Ala Val Leu Ala Glu Glu Thr His Asn Phe Gly Leu
159 225           230          235          240
161 Asn Phe Leu Gln Thr Ile Lys Gly Lys Ile Val Ser Lys Gln Lys Leu
162           245          250          255
164 Glu Leu Lys Thr Thr Glu Ala Gly Pro Arg Leu Met Ser Gly Lys Gln
165           260          265          270
167 Ala Ala Ala Ile Ile Lys Ala Val Asp Ser Lys Tyr Thr Ala Ile Pro
168           275          280          285
170 Ile Val Gly Gln Val Phe Gln Ser His Cys Lys Gly Cys Pro Ser Leu
171           290          295          300
173 Ser Glu Leu Trp Arg Ser Thr Arg Lys Tyr Leu Gln Pro Asp Asn Leu
174 305           310          315          320
176 Ser Lys Ala Glu Ala Val Arg Asn Phe Leu Ala Phe Ile Gln His Leu
177           325          330          335
179 Arg Thr Ala Lys Lys Glu Glu Ile Leu Gln Ile Leu Lys Met Glu Asn
180           340          345          350
182 Lys Glu Val Leu Pro Gln Leu Val Asp Ala Val Thr Ser Ala Gln Thr
183           355          360          365
185 Ser Asp Ser Leu Glu Ala Ile Leu Asp Phe Leu Asp Phe Lys Ser Asp

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186      370      375      380
188 Ser Ser Ile Ile Leu Gln Glu Arg Phe Leu Tyr Ala Cys Gly Phe Ala
189 385      390      395      400
191 Ser His Pro Asn Glu Glu Leu Leu Arg Ala Leu Ile Ser Lys Phe Lys
192      405      410      415
194 Gly Ser Ile Gly Ser Ser Asp Ile Arg Glu Thr Val Met Ile Ile Thr
195      420      425      430
197 Gly Thr Leu Val Arg Lys Leu Cys Gln Asn Glu Gly Cys Lys Leu Lys
198      435      440      445
200 Ala Val Val Glu Ala Lys Lys Leu Ile Leu Gly Gly Leu Glu Lys Ala
201      450      455      460
203 Glu Lys Lys Glu Asp Thr Arg Met Tyr Leu Leu Ala Leu Lys Asn Ala
204 465      470      475      480
206 Leu Leu Pro Glu Gly Ile Pro Ser Leu Leu Lys Tyr Ala Glu Ala Gly
207      485      490      495
209 Glu Gly Pro Ile Ser His Leu Ala Thr Thr Ala Leu Gln Arg Tyr Asp
210      500      505      510
212 Leu Pro Phe Ile Thr Asp Glu Val Lys Lys Thr Leu Asn Arg Ile Tyr
213      515      520      525
215 His Gln Asn Arg Lys Val His Glu Lys Thr Val Arg Thr Ala Ala Ala
216      530      535      540
218 Ala Ile Ile Leu Asn Asn Asn Pro Ser Tyr Met Asp Val Lys Asn Ile
219 545      550      555      560
221 Leu Leu Ser Ile Gly Glu Leu Pro Gln Glu Met Asn Lys Tyr Met Leu
222      565      570      575
224 Ala Ile Val Gln Asp Ile Leu Arg Leu Glu Met Pro Ala Ser Lys Ile
225      580      585      590
227 Val Arg Arg Val Leu Lys Glu Met Val Ala His Asn Tyr Asp Arg Phe
228      595      600      605
230 Ser Arg Ser Gly Ser Ser Ser Ala Tyr Thr Gly Tyr Ile Glu Arg Ser
231      610      615      620
233 Pro Arg Ser Ala Ser Thr Tyr Ser Leu Asp Ile Leu Tyr Ser Gly Ser
234 625      630      635      640
236 Gly Ile Leu Arg Arg Ser Asn Leu Asn Ile Phe Gln Tyr Ile Gly Lys
237      645      650      655
239 Ala Gly Leu His Gly Ser Gln Val Val Ile Glu Ala Gln Gly Leu Glu
240      660      665      670
242 Ala Leu Ile Ala Ala Thr Pro Asp Glu Gly Glu Glu Asn Leu Asp Ser
243      675      680      685
245 Tyr Ala Gly Met Ser Ala Ile Leu Phe Asp Val Gln Leu Arg Pro Val
246      690      695      700
248 Thr Phe Phe Asn Gly Tyr Ser Asp Leu Met Ser Lys Met Leu Ser Ala
249 705      710      715      720
251 Ser Gly Asp Pro Ile Ser Val Val Lys Gly Leu Ile Leu Leu Ile Asp
252      725      730      735
254 His Ser Gln Glu Leu Gln Leu Gln Ser Gly Leu Lys Ala Asn Ile Glu
255      740      745      750
257 Val Gln Gly Gly Leu Ala Ile Asp Ile Ser Gly Ala Met Glu Phe Ser
258      755      760      765

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264 785      790      795      800
266 Leu Glu Thr Ser Thr Glu Thr Glu Ala Gly Leu Glu Phe Ile Ser Thr
267      805      810      815
269 Val Gln Phe Ser Gln Tyr Pro Phe Leu Val Cys Met Gln Met Asp Lys
270      820      825      830
272 Asp Glu Ala Pro Phe Arg Gln Phe Glu Lys Lys Tyr Glu Arg Leu Ser
273      835      840      845
275 Thr Gly Arg Gly Tyr Val Ser Gln Lys Arg Lys Glu Ser Val Leu Ala
276      850      855      860
278 Gly Cys Glu Phe Pro Leu His Gln Glu Asn Ser Glu Met Cys Lys Val
279 865      870      875      880
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282      885      890
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286 <211> LENGTH: 2878
287 <212> TYPE: DNA
288 <213> ORGANISM: Mus musculus
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293 ctatacaagc tcacgtactc cactgaagtg tttcttgatg ggggcaaaag aaaaccgcaa 180
294 gacagcgtgg gctacaaaat ctcatctgat gtggacgttg tgttactgtg gaggaatcct 240
295 gatggtgatg atgatcaagt gatccaagtc acgataacag ctgttaacgt tgaaaatgcg 300
296 ggtaacacaga gaggcgagaa gagcatcttc cagggcaaaa gtacaccta gacatagggg 360
297 aaggacaacc tggaggctct gcagagaccc atgcttcttc atctggtccg ggggaagggtc 420
298 aaggagtctt actcctatga aaacgagcca gtgggcatag aaaatctcaa gagaggcttg 480
299 gctagcttat tccagatgca gctaagctct ggaactacca acgaggtaga tatctctggg 540
300 gattgtaaag tgacctacca ggccaacaa gacaaagtgg tcaaaattaa ggctctggat 600
301 acatgcaaaa ttgagcgggtc tggatttaca acggcaaaacc aggtgctggg cgctcagttca 660
302 aaagccacat ctgtcactac ctacaagata gaggacagct ttgtcaccgc tgtgcttgca 720
303 gaagagacca gggcttttgc cttgaacttc caacaaacca tagcaggaaa aatagtgtca 780
304 aagcagaaat tggagctgaa gacaactgaa gccggcccaa ggatgatccc cgggaagcaa 840
305 gtggcagggtg taattaaagc agttgattcc aaatacaaag ccattcccat tgtgggacag 900
306 gtcctcgagc gtgtctgcaa aggatgccct tctctggcgg agcactggaa gtccatcaga 960
307 aagaacctgg agcctgaaaa cctgtccaag gccgaggctg tccagagctt cctggccttc 1020
308 atccagcacc tccggacttc gaggagagaa gagatcctcc agattctgaa ggcagagaag 1080
309 aaagaagtgc tccctcagct ggtggatgcc gtcacctctg ctgagactcc agactcgcta 1140
310 gaagccatcc tggacttttt ggatttcaaa agtgacagca gtatcatact ccaggaaagg 1200
311 ttcctctatg cctgtggctt tgccacccac cctgatgaag aactcctacg agccctcctt 1260
312 agtaagttca aaggttcctt tgcaagcaac gacatcagag agtcggttat gatcatcatt 1320
313 ggagccctag tcaggaagct gtgtcagaat gaaggctgca agctcaaggc agtgggtgaa 1380
314 gctaagaagc tgatcctggg aggacttgaa aaaccagaga agaaaaga caccacaatg 1440
315 tacctgcttg ccctgaagaa tgccttgctt cccgaaggca tcccgctcct tctgaagtat 1500
316 gctgaggctg gagaagggcc cgtcagccac ctgggccacca ctgttctcca gagatacgat 1560
317 gtctccttca tcacagatga ggtgaagaag accttgaaca ggatatacca ccagaatcgt 1620
318 aaggttcatg agaagacggt gcgcacaact gccgctgctg tcatcttaaa gaacccatcc 1680

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 14,16,27,31,36,43,47,50,52,53,70,77,81,95,121,123,130,171
Seq#:11; Xaa Pos. 177,180,197,200,203,204,226,233,241,243,248,261
Seq#:12; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165
Seq#:12; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268
Seq#:12; Xaa Pos. 270,275,287
Seq#:13; Xaa Pos. 6,16,17,46,48,51,54,55,63,69,81,84,89,95,97,105,108,133
Seq#:13; Xaa Pos. 140,142,149,155,162,163,174,176,177,180,191,193,198,202
Seq#:14; Xaa Pos. 35,41,52,57,58,59,70,72,77,81,82,97,104,108,109,118,126
Seq#:14; Xaa Pos. 128,131,149,157,166,186,189,195,200,210,219,222,240,252
Seq#:14; Xaa Pos. 253,261,273,274,297
Seq#:15; Xaa Pos. 57,67,68,97,99,102,105,106,116,122,149,152,157,163,165
Seq#:15; Xaa Pos. 173,176,207,214,216,223,229,239,240,251,253,254,257,268
Seq#:15; Xaa Pos. 270,275,287
Seq#:16; Xaa Pos. 43,49,60,65,66,67,78,80,85,89,90,105,112,116,117,126,134
Seq#:16; Xaa Pos. 136,139,157,165,174,194,197,203,208,227,236,239,257,269
Seq#:16; Xaa Pos. 270,278,290,291,292,314

VERIFICATION SUMMARY

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L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48
M:341 Repeated in SeqNo=12
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:32
M:341 Repeated in SeqNo=14
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48
M:341 Repeated in SeqNo=15
L:921 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:32
M:341 Repeated in SeqNo=16